

Figure 1.

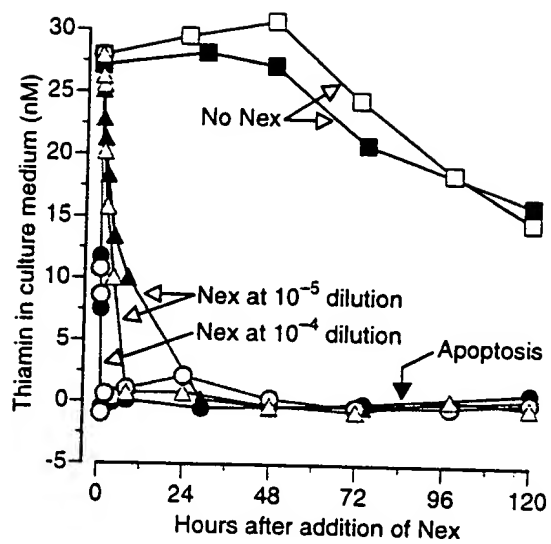


Figure 2.

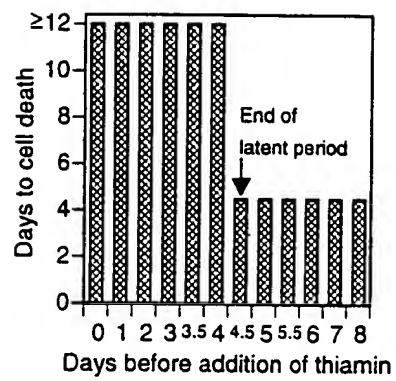


Figure 3.

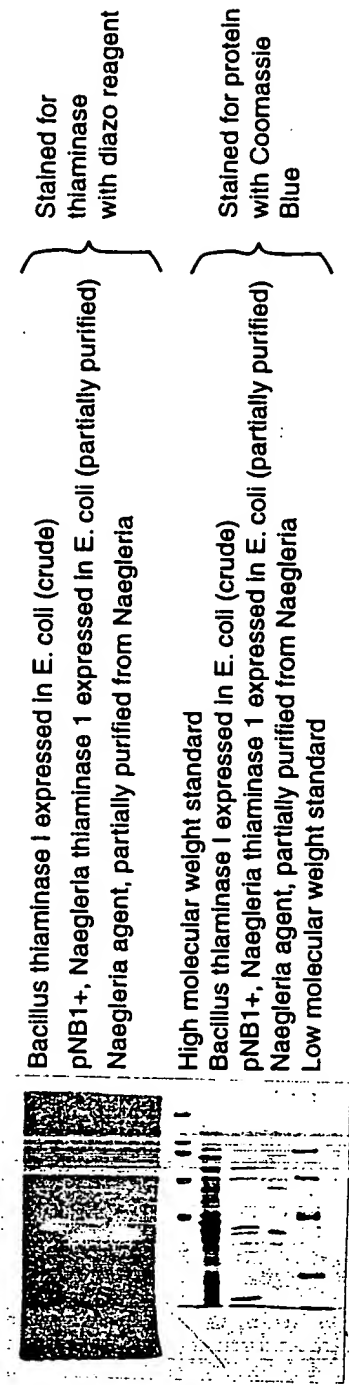


Figure 4.

(SEQ ID NO: 1)

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1   ATGTCCACTC AACCAAAGAC ACTCACTGTT GGTCTCTTCC CATATCTTCC TTCTTGGAAT
61  GAAAATGGCA ACGAAGTTAA ATTGATCAAT TTGATCAAGG ATGTTTTGCC AACTCAGGTT
121 TCCGGATATA ATATCGAATA TACCGAATTT GATTGTTACA GTGATGCTAG TCTTCAAAGT
181 CTTCCAGATG TTTTCTCAAC TGATAGCATT TTCCTTCCAT ATCTTGTTTC TTTGGGTGGT
241 GTCAAGAGTT TGGATGAATC ATTGGTTCGT GGTGTTACTG GTGATTTGCA TAGTTTTGTT
301 TCCTCAAGTG CCTCTGTCAA TGGTTCGGTT TATGGTTTCC CACAATACTT GTGCTCAAAC
361 TTTTATTGT CCTCACCAA TGGTACTCAA CAAGCATCTT CCCTTTTAGA ATTGGCTCAA
421 AAGGTTGGTT ATGAACAAAT TGTTTATCCA GATGTTGCCT CTTCTAGTTC TTTCACAGTT
481 TTCGGATTGT ATCAACAATT ACTCCAATCA TCATCATCAG CTGCAGTTGA TATCAAGGCC
541 TCTGATCTTC CACAATCTGG TGACCAAGTC AACAAGGATA TCACTCAAAA ATATAGAACC
601 ATTTTGGATT CAACAGTTGT TGCCTCTCAA AGAGAATATA TTAACCTCTGT AAAGCAAGGT
661 AAACCAATTT CAAACTACTA TGTCGGATAT AGTGAAAGTA TGTGTGAAAT TAAGGATATC
721 ATCAGAGATC AACAAATACAA TGTTCAACTC ATTGGTACCT CTGATAAGCC ATACGTTTAT
781 ACTGATGTTT TGGCTTTGAA TTCCAATTTG TGTGATGAAA AGCAAAAGGT TGCTGTTGAA
841 GTTATCAAGA ATTTATTGAC TAATACTTTA GTTTTGGACT TGTGAGGCTC CGGATTAACCT
901 CTCCCAGCCA ACAAGAATGG TATTGCTCAT TTGGCTAAAT CATCAAACCT TTATGCTCAA
961 TTGAGCCAAC AATTCGATGC CAAGGAAAGT GAAGTTAGAG TTTTGAGATG TGTTGACTTT
1021 GCTAACCAAG AAGTTAAGAA TTGTGCTGGT GTCTTGAGAC CATTCTTCA ACATATTGCT
1081 GTTGCTACTT TGCCTTGTTC GACTGCTGAC ACTGTGCGAA AGGCTAAGAG TGGTCACCCT
1141 GGTATGCCAA TTGGTATGTC ACCAATTGCC TATGTTTTGT GGAAGTTCTT CTTCAAATCA
1201 TCTAAGGATG ATGTCAATTG GTTGAACAGA GATAGATTGT TTTTGAGTAA TGGTCACGGT
1261 TGACATTGC TTTATGCCAT GTTGCACCTC ACTGATTGTA ACTTGAGTTT GGATGATCTC
1321 AAGAATTTCA GAAGTTTGCA TTCCAAGACT CCTGGTCACC CAGAATATGG TCACACTGAA
1381 GGTGTTGATG CTACTACTGG TCCATTGGGT CAAGGTGTTT GTAATGCTAT TGGTATGGCT
1441 CTCTCTGAAG CTCACCTGGC TGCTCGTTTC AATAAGGATG GACAAAATAT CTTTGATCAC
1501 CACACCTATG TTTTCCTTGG TGATGGTTGT TTGATGGAAC GTGTTGCTAT GGAAGGTCTC
1561 TCATTTGCTG GTCACCAAAA GTTGAACAAG TTGATTGTTT TCTATGATGA CAATAGTATT
1621 ACTATTGATG GTAAGACTGA ATTGACCTTT ACTCAAAATA CTCCAGAAGT CATGAGAGGT
1661 TTTGGATGGC ACGTAATTGT TGTCGACAAG GCTGATAATG ACTTGGTTGG TATTAAGGAA
1721 GCTATTTTGG AAGCTCACAC TGTTACTGAC AAGCCAATCA TGATCGTTTG TAAGACTACA
1781 ATTGGTTATT CCTCAAAGGT TCAAGGTACT GCTAAGGTTT ACGGTTCTCC ATTGGGTGCT
1841 GATGGATTGA AGAATTTGAA GGAAACTTGT GGTTCCTACT GTAATGATT CTTCCATGTT
1901 CCAGAAATTG TCAGAAAGGA CTTTGCTACT GTCATTAATA GAAATAGTGA AAAGCTCTCT
1961 CAATGGAAGC AAGTTAAATC TGCCATATGAT ACCACTCATG CTACTGAATC CCAACTCCTC
2021 CAAAGAATGA TTAATCACGA ATTGGAAGGT GATGTTATGG AAAAGTTGCC AAAATACCTC
2081 GAACAAAAGA AGATTGCTAC CAGATCTACA TCTCAACAAG TTTTGAATGC CATCTATCCA
2141 CTCATTCTTT CTCTCGTTGG TGGTTCAGCT GACTTGACTC CATCCAACCT GACTGATGTA
2201 ACTGGATGTC AAGATTTCCA ACCAAACAAT AGAGTTGGTA GATATATCAG ATTTGGTGTC
2261 CGTGAACATG CCAATGGTTGC TATTGCCAAT GGTATTCTCT ATCATGGTGT TCTTAGAACC
2321 TATGTTGGTA CATTCTTGAA CTTTGCTTCA TATGCTTTGG GTGCTATCAG ATTGAGTGCC
2381 TTGTCTGGTC TTCCAAATAT TTATGTTTTT ACTCATGACA GTATTGGTCT TGGTCAAGAT
2441 GGTCCAACCT ACCAACCTGT TGAAGTTTGA CCAATGTTGA TAGCCATTCC AAATCACATT
2521 GTTTTCAGAC CTGCTGATGG TAGAGAAACC AGTGGTGCTT ATTTGTGGGC TGTTCATCA
2581 AAGAAGACTC CATCCTCAAT GATTCTTTCT CGTCAAGATT TGCCACAATT GACTGGTACT
2641 GATATTTCAA AGGTGCTTTT GGGTGCCTAT GTTATCCAAG GTGATGCTAC TCCTGATGTT
2701 GTCCTTGTTG GACTGCTTTC TGAAGTTTCC CTGATGGTTG AAGCTGCTGA AAGCTGCTGA
2761 GCTAACCTTA AGGTTAACGT TGTTTCCATG CCAAGTTGGG AATTGTTTGT TCGTCAATCA
2821 GAAGAATACA GGAAGACTGT CTTCCCAGAT GGTATTCCAG TTGTCAGTGC CGAAGCTTCA
2881 TCAACCTTTG GTTGGAACAAG CTTTGCTCAC TATGCTGTTG GTATGACTAC TTTCCGTGCT
2941 AGTGCTGCTG CTGAAGAAGT TTACAAACTC CTCAAGATTA CCTCAGACAA TGTTGCTGAA
3001 AAGGCCACCA AATTGGTTAC CAAGTATGGT AAGCAAGCTC CAAGACTCAG CTTGTCTCTT
3061 GTTGGTGAAG AACTCTAA

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Figure 5.

(SEQ ID NO: 2)

MSTQPKTLTVGLFPYLPSWNENGNEVKLINLIKDVLPQTQVSGYNIEYTEFDCYSDASLQSLPDVFSTDSIFLPYLVSLGG
VKSLDESLVRGVTGDLHSFVSSSASVNGSVYGFPPQYLCNFFLLSSPNGTQQASSLLELAQKVGYEQIVYPDVASSSSFTV
FGLYQQLLQSSSSAAVDIKASDLPOSGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYYVGYSESMCEIKDI
IRDQQYNVQLIGTSDKPYVYTDVLALNSNLCDEKQKVAVEVIKNLLTNTLVLDLLGLGLTLPANKNGIAHLAKSSNFYAQ
LSQQFDAKESEVRVLRVDFANKEVKNCAGVLRPFLQHIATLRCLTADTVEKAKSGHPGMPIGMSPIAYVLWKFFFKS
SKDDVNWLNRRDRFVLSNGHGCTLLYAMLHLTDCNLSLDDLKNFRSLHSKTPGHPEYGHTEGVDATTGPLGQGVCAIGMA
LSEAHLAARFNKDGQNI FDHHTYVFLGDGCLMERVAMEGLSFAGHQKLNKLIVFYDDNSITIDGKTELTFTQNTPEVMRG
FGWHVIVVDKADNDLVGIKEAILEAHTVTDKPIMIVCKTTIGYSSKVQGTAKVHGSPLGADGLKNLKETCGFTGNDFFHV
PEIVRKDFATVINRNSEKLSQWKQVKSAYDTTHATESQLLQRMINELEGDVMEKLPKYLEQKKIATRSTSQQVLNAIYP
LIPSLVGGSSADLTPSNLTDVTGCQDFQPNNRVGRYIRFGVREHAMVAIANGILYHGVLRTYVGTFLNFASYALGAIRLSA
LSGLPNIIYVFTHDSIGLGQDGPTHQPVEVLPMLIAIPNHIVFRPADGRETSAYLWAVQSKKTPSSMILSRQDLPLTGT
DISKVALGAYVIQGDATPDVVLVGTGSEVSLMVEAAEKLKANLKVNVVSMPSWELFVRQSEYRKTVPDGPVVSAAES
STFGWTSFAHYAVGMTTFGASAAAEVYKLLKITS DNVAEKATKLVTKYKGQAPRLSLSLVGEEL

Figure 6.

(SEQ ID NO: 3)

ATGTCCACTCAACCAAGACACTCACTGTTGGTCTCTTCCCATATCTTCTTCTTGAATGAAAATGGCAACGAAGTTAA
ATTGATCAATTTGATCAAGGATGTTTTGCCAACTCAGGTTTCCGGATATAATATCGAATATACCGAATTTGATTGTTACA
GTGATGCTAGTCTTCAAAGTCTTCCAGATGTTTTCTCAACTGATAGCATTTCCTTCCATATCTTGTTTCTTTGGGTGGT
GTCAAGAGTTTGGATGAATCATTGGTTCGTGGTGTACTGGTGATTGTCATAGTTTGTTCCTCAAGTGCCTCTGTCAA
TGGTTCGGTTTATGGTTTCCCACTACTTGTGCTCAAACCTTTTTATTGTCCTCACCAAATGGTACTCAACAAGCATCTT
CCCTTTTAGAATTGGCTCAAAGGTTGGTTATGAACAAATTGTTTATCCAGATGTTGCCTCTTCTAGTTCTTTCACAGTT
TTCGGATTGTATCAACAATTACTCCAATCATCATCATCAGCTGCAGTTGATATCAAGGCCTCTGATCTTCCACAATCTGG
TGACCAAGTCAACAAGGATATCACTCAAAAATATAGAACCATTTTGGATTCAACAGTTGTTGCCTCTCAAAGAGAATATA
TTAACTCTGTAAAGCAAGGTAAACCAATTTCAAACCTACTATGTCGGATATAGTGAAAGTATGTGTGAAATTAAGGATATC
ATCAGAGATCAACAATACAATGTTCAACTCATTGGTACCTCTGATAAGCCATACGTTTATACTGATGTTTTGGCTTTGAA
TTCCAATTTGTGTGATGAAAAGCAAAAGGTTGCTGTTGAAGTTATCAAGAATTTATTGACTAATACTTTAGTTTTGGACT
TGTTGGGTCTCGGATTAACTCTCCAGCCAACAAGAATGGTATTGCTCATTGGCTAAATCATCAAACCTTTTATGCTCAA
TTGAGCCAACAATTCGATGCCAAGGAAAGTGAAGTTAGAGTTTTGAGATGTGTTGACTTTGCTAACAAGGAAGTTAAGAA
TTGTGCTGGTGTCTTGAGACCATTTCCTT

Figure 7. (SEQ ID NO: 3/SEQ ID NO: 4)

1/1 31/11
 ATG TCC ACT CAA CCA AAG ACA CTC ACT GTT GGT CTC TTC CCA TAT CTT CCT TCT TGG AAT
 Met ser thr gln pro lys thr leu thr val gly leu phe pro tyr leu pro ser trp asn

61/21 91/31
 GAA AAT GGC AAC GAA GTT AAA TTG ATC AAT TTG ATC AAG GAT GTT TTG CCA ACT CAG GTT
 glu asn gly asn glu val lys leu ile asn leu ile lys asp val leu pro thr gln val

121/41 151/51
 TCC GGA TAT AAT ATC GAA TAT ACC GAA TTT GAT TGT TAC AGT GAT GCT AGT CTT CAA AGT
 ser gly tyr asn ile glu tyr thr glu phe asp cys tyr ser asp ala ser leu gln ser

181/61 211/71
 CTT CCA GAT GTT TTC TCA ACT GAT AGC ATT TTC CTT CCA TAT CTT GTT TCT TTG GGT GGT
 leu pro asp val phe ser thr asp ser ile phe leu pro tyr leu val ser leu gly gly

241/81 271/91
 GTC AAG AGT TTG GAT GAA TCA TTG GTT CGT GGT GTT ACT GGT GAT TTG CAT AGT TTT GTT
 val lys ser leu asp glu ser leu val arg gly val thr gly asp leu his ser phe val

301/101 331/111
 TCC TCA AGT GCC TCT GTC AAT GGT TCC GTT TAT GGT TTC CCA CAA TAC TTG TGC TCA AAC
 ser ser ser ala ser val asn gly ser val tyr gly phe pro gln tyr leu cys ser asn

361/121 391/131
 TTT TTA TTG TCC TCA CCA AAT GGT ACT CAA CAA GCA TCT TCC CTT TTA GAA TTG GCT CAA
 phe leu leu ser ser pro asn gly thr gln gln ala ser ser leu leu glu leu ala gln

421/141 451/151
 AAG GTT GGT TAT GAA CAA ATT GTT TAT CCA GAT GTT GCC TCT TCT AGT TCT TTC ACA GTT
 lys val gly tyr glu gln ile val tyr pro asp val ala ser ser ser ser phe thr val

481/161 511/171
 TTC GGA TTG TAT CAA CAA TTA CTC CAA TCA TCA GCT GCA GTT GAT ATC AAG GCC
 phe gly leu tyr gln gln leu leu gln ser ser ser ala ala val asp ile lys ala

541/181 571/191
 TCT GAT CTT CCA CAA TCT GGT GAC CAA GTC AAC AAG GAT ATC ACT CAA AAA TAT AGA ACC
 ser asp leu pro gln ser gly asp gln val asn lys asp ile thr gln lys tyr arg thr

601/201 631/211
 ATT TTG GAT TCA ACA GTT GTT GCC TCT CAA AGA GAA TAT ATT AAC TCT GTA AAG CAA GGT
 ile leu asp ser thr val val ala ser gln arg glu tyr ile asn ser val lys gln gly

661/221 691/231
 AAA CCA ATT TCA AAC TAC TAT GTC GGA TAT AGT GAA AGT ATG TGT GAA ATT AAG GAT ATC
 lys pro ile ser asn tyr tyr val gly tyr ser glu ser met cys glu ile lys asp ile

721/241 751/251
 ATC AGA GAT CAA CAA TAC AAT GTT CAA CTC ATT GGT ACC TCT GAT AAG CCA TAC GTT TAT
 ile arg asp gln gln tyr asn val gln leu ile gly thr ser asp lys pro tyr val tyr

781/261 811/271
 ACT GAT GTT TTG GCT TTG AAT TCC AAT TTG TGT GAT GAA AAG CAA AAG GTT GCT GTT GAA
 thr asp val leu ala leu asn ser asn leu cys asp glu lys gln lys val ala val glu

841/281 871/291
 GTT ATC AAG AAT TTA TTG ACT AAT ACT TTA GTT TTG GAC TTG TTG GGT CTC GGA TTA ACT
 val ile lys asn leu leu thr asn thr leu val leu asp leu leu gly leu gly leu thr 1

901/301 931/311
 CTC CCA GCC AAC AAG AAT GGT ATT GCT CAT TTG GCT AAA TCA TCA AAC TTT TAT GCT CAA
 leu pro ala asn lys asn gly ile ala his leu ala lys ser ser asn phe tyr ala gln

961/321 991/331
 TTG AGC CAA CAA TTC GAT GCC AAG GAA AGT GAA GTT AGA GTT TTG AGA TGT GTT GAC TTT
 leu ser gln gln phe asp ala lys glu ser glu val arg val leu arg cys val asp phe

1021/341 1051/351
 GCT AAC AAG GAA GTT AAG AAT TGT GCT GGT GTC TTG AGA CCA TTC CTT
 ala asn lys glu val lys asn cys ala gly val leu arg pro phe leu

Figure 8-1.

Abbrev.	Genbank	Enzyme and Organism
ScTKT1ct	- P23254	Transketolase of <i>Saccharomyces cerevisiae</i>
CpTKT7ct	- Q42677	Transketolase of <i>Craterostigma plantagineum</i>
EcTKT2ct	- P33570	Transketolase of <i>Escherichia coli</i>
BsTKTct	- P45694	Transketolase of <i>Bacillus subtilis</i>
MgTKT	- P47312	Transketolase of <i>Mycoplasma genitalium</i>
MjPTK1	- Q58092	Transketolase of <i>Methanococcus jannaschii</i>
BSTP	- P45741	Thiaminase I precursor from <i>Bacillus thiaminolyticus</i>
N40KAT	- ----->	Thiaminase I of <i>Naegleria gruberi</i> , aa 1-356

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ScTKT1ct      ADDVK---QLKSKFGFNPDKSFVVPQEVYD-HYQKTILKPGVEANNKWNKLFSEYQKKFP      56
CpTKT7ct      PKEAE---ATRKNLGW-PYEPFHPVDDVKK-HWSRHIAE-GAALESANNAKFAEFQKKFP
EcTKT2ct      EEEVA---LARQKLGW-HHPPFEIPKEIY--HAWDAREK-GEKAQQSWNEKFAAYKKAHP
BsTKTct       KEESK---LTKEAYAWTYEEDFYVPSEVYE-HFAVAVKESGEKKEQEWNAQFAKYKEVYP
MgTKT         EVDFQ---LFEKRTNT-NFNFFNYPDSIYH-WFKQTVIERQKQIKEDYNLLISLKD-K-P
MjPTK1        -----
BsTP          MSKVKGFIYKPLMVMLALLLVVSPAGAGAAHSDASSDITLKVAIYPYVPDPAFQA AVL
N40KAT        MSTQP----KTLTVGLFPYL----PS-----WNENGNEVKLINLIKDVLP-----

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ScTKT1ct      ELGAELARRLSGQLPANWESKLPTYTAKDSA---VATRKLSETVLEDVYNQLPELIGGS      112
CpTKT7ct      EEAADLKSIIITGELPTNWESIFPTYTPENPG---LPTRTLSHQILNGLGDVLPGLLGGS
EcTKT2ct      QLAEETFRRMSGGLPKDWEKTQKYINELQANPAKIATRKASQNTLNAYGPMLELLGGS
BsTKTct       ELAEQLELAIKGELPKDWDQEVVPYE-KGSS---LASRASSGEVLNGLAKKIPFFVGGS
MgTKT         -LFFKFTNWIDSDFQALYLNQLDEKKVAKD---SATRNYLKDFLNQINNPNNSNLYCLN
MjPTK1        -----MVKLSGVYKG-----MRKGYGETLIELGKKYENLVVLD
BsTP          DQWQRQEPGVKLEF-TDWDYSADPPDDL DV---FVLDSIFLSHFVDAGYLLP-FGSQD
N40KAT        -----QVSGYNIEY-TEFDCYSDASLQSLPD---VFSTDSIFLPYLVSLGGVKS LDES LV

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ScTKT1ct      ADLTPSNLTRWKEALDFQPPSSSGSGNYSGRYIRYGIREHAMGA---IMNGISAFGANYKPYGG      172
CpTKT7ct      ADLTLNMAFLKNSGDFQKKSPGE-----RNVKFGAREHAMGS---ICNGLALHSPGLLPYCA
EcTKT2ct      ADLAPSNLTIWKGSVSLKEDPAGN-----YIHGVREFGMTA---IANGIAHHG-GFVPTYA
BsTKTct       ADLAGSNKTTIKNAGDFTAVDYSG-----KNFWFGVREFAMGA---ALNGMALHG-GLRVFGG
MgTKT         ADVSRS--CFIKIGDDNLHENPCS-----RNIQIGIREFAMAT---IMNGMALHG-GIKVMGG
MjPTK1        ADLSGS-----TQTAMFAKEFPE-----RFFNAGVAEQNMIG---MAAGLAT TG--KIVFAS
BsTP          IDQAEDVLPFALQGA KRNGEVYGLP-----QILCTNLLFYRKGD LKIGQVDNIYELYKKIG
N40KAT        RGVTDGLHSFVSSSASVNGSVYGF P-----QYLCSNFL LSS---PNGTQQAS-SLLELAQ

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Catalytic Cys

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ScTKT1ct      TFLNFVS-YAAGAVR-LSALSGHPVIWVATHDSIGV-GE---DG-PTHQPIET--LAHF      222
CpTKT7ct      TYFVFTD-YMRAAMR-ISALSKARVLYIMTHDSIGL-GE---DG-PTHQPVEH--LASF
EcTKT2ct      TFLMFVE-YARNAAR-MAALMKARQIMVYTHDSIGL-GE---DG-PTHQAVEQ--LASL
BsTKTct       TFFVFSD-YLRPAIR-LAALMGLPVTVVFTHDSIAV-GE---DG-PTHEPVEQ--LASL
MgTKT         TFLAFAD-YSKPAIR-LGALMNLPVFVYVYTHDSYQV-GG---DG-PTHQPYDQ--LPML
MjPTK1        SFSMFASGRAWEIIRNLVAYPKLNVKIVATHAGITV-GE---DG-ASHQMCED--IAIM
BsTP          TSHSEQIPPPQNKGLLINMAGGTTKASMYLEALIDVTGQYTEYDLLPPLDPLNDK VIRGL
N40KAT        KVGYEQIVYPDVASSSSFTVFGLYQQLLQSSSSAAV-----DIKASDLPQSGD-QVNK

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*
(SEQ ID NO: 12) Peptide A -> ASDLPQSGD-QVNK

Figure 8-2.

ScTKT1ct	RSLPNIQVWRPADGN-EVSAAYKNSLESKHTPSIIALSRQNLPOLEGS--- <td>278</td>	278
CpTKT7ct	RAMPNILTLPADGN-ETAGAYRAAVQNGERPSILVLARQKLPLPGT--- <td></td>	
EcTKT2ct	RLTPNFSTWRPCDQV-EAAVGVKLAVERHNGPTALILSRQNLQAVERTPD-QVKEIARGG	
BsTKTct	RAMPNLSLIRPADGN-ETAAAWKLAVQSTDHPTALVLTRQNLPTIDQTSEEALAGVEKGA	
MgTKT	RAIENVCVFRPCDEK-ETCAGFNYGLLSQDQTTVLVLTRQPLKSIDNTD--SLKTL-KGG	
MjPTK1	RAIPNMVVIAPTYY-HTKNVIRTIAEYKG-PVYVRMPRRDTEIIYENEEETFEIGKKG	
BsTP	RLLINMAGEKPSQYVPEDGDAYVRASWFAQ-GSGRAFIGYSESMMRMG---DYAEQVRFK	
N40KAT	DITQKYRTILDSTVV-ASQREYINSVKQKG-PISNYVVGYSSEMCEIK---DIIRDQQYN	

Peptide B -> TILDSTVV-ASQR (SEQ ID NO: 13)

ScTKT1ct	YVLQDVAN-----PDIILVATGSEVSLSVEAAKTAAKNIKARVVSLPDFFTFDKQPLE-	332
CpTKT7ct	YVISDN\$RGGSNKPDVILIGTGSELEIAARAGDELRKEGKKVRVSVLVCWELFAEQSEK-	
EcTKT2ct	YVLKDSGG----KPDILIIATGSEMEITLQAAEKLAGEGRNVRVSVLPSTDI FDAQDEE-	
BsTKTct	YVVSXSKN--E-TPDALLIASGSEVGLAIEAQAE LAKENIDVSVVSMPSMDRFEKQSDE-	
MgTKT	YILLDRKQ-----PDLIIAASGSEVQLAIEFEKVLTKQNVKVRILSVPNITLLLKQDEK-	
MjPTK1	ILVDG-----EDLTI IATGEEVPEALRAGEILKENGISAEIVEMATIKPIDEEI IKK	
BsTP	PISSSAG-----QDIPLFYSDVSVNSKTAHPELAKKLANVMASADTVEQALRPQADGQ	
N40KAT	VQLIGTS-----DKPYVYTDVLALNSN---LCDEKQKVAVEVIKNLLTNTLVLDLLG-	

ScTKT1ct	YRLSVLPDNPVI-MSVEVLATTCWGKYAH-----QSFIDRFGASGKAPEVFKFFGFTP	385
CpTKT7ct	YRETVLP\$GVTARVSVEAGSTFGWERFIGP-KG--KAVGIDRFGASAPAERLFKEFGITV	
EcTKT2ct	YRESVLPSNVAARVAVEAGIADYWKYVGL-KG--AIVGMTGYGESAPADKLFPPFGFTA	
BsTKTct	YKNEVLPADVKKRLAIEMGSSFGWGKYTGL-EG--DVLGIDRFGASAPGETI INEYGF\$V	
MgTKT	YLKSLFDANSSL-ITIEASSSYEWFCFKKY-VKNHAHLGAF\$FGESDDGDKVYQKGFNL	
MjPTK1	SKDFVVTVEDHSIIGGLGGAVA\$VIASNGLNKKLLRIGINDVFGRS\$KADELLKYYGLDG	
BsTP	YPQYLLPARHQV-YEALMQDYPIYSELAQIVNK--PSNRVFR\$GPEVRT-WLKDAKQVLP	
N40KAT	-LGLTLPANKNG-IAHLAKSSNFYAQLSQ-----QFDAKESEVRVLR\$VDFANKEV	

Peptide C -> SSNFYAQLSQ-----QFDAK (SEQ ID NO: 14)

ScTKT1ct	EGVAERAQKTIAFYKGDKLISPLKKAF	412	(SEQ ID NO: 5)
CpTKT7ct	EAVVA-AAKEIC-----		(SEQ ID NO: 6)
EcTKT2ct	ENIVAKAHKVLGVKGA-----		(SEQ ID NO: 7)
BsTKTct	PNVVNRVKALINK-----		(SEQ ID NO: 8)
MgTKT	ERLMKIFTSLRN-----		(SEQ ID NO: 9)
MjPTK1	ESIAKRIMEEMKKE-----		(SEQ ID NO: 10)
BsTP	EALGLTDVSSLAS-----		(SEQ ID NO: 11)
N40KAT	KNCAGVLRPFL-----		(SEQ ID NO: 4)